

#8



SEQUENCE LISTING

<110> Bayne, Marvin L.
Conn, Gregory L.
Thomas, Jr., Kenneth A.

<120> VASCULAR ENDOTHELIAL CELL GROWTH FACTOR
II

<130> 18199CB

<140> US 10/071,370

<141> 2002-02-08

<150> 09/326,879

<151> 1999-06-07

<150> 09/038,199

<151> 1998-03-10

<150> 08/299,185

<151> 1994-08-31

<150> 08/000,834

<151> 1993-01-05

<150> 07/586,638

<151> 1990-09-21

<160> 29

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 577

<212> DNA

<213> rat

<220>

<221> CDS

<222> (5)...(577)

<400> 1

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	Met	Asn	Phe	Leu	Leu	Ser	Trp	Val	His	Trp	Thr	Leu	Ala	Leu	Leu	
	1				5				10					15		

ctg	tac	ctc	cac	cat	gcc	aag	tgg	tcc	cag	gct	gca	ccc	acg	aca	gaa	97
Leu	Tyr	Leu	His	His	Ala	Lys	Trp	Ser	Gln	Ala	Ala	Pro	Thr	Thr	Glu	
				20				25						30		

ggg	gag	cag	aaa	gcc	cat	gaa	gtg	gtg	aag	ttc	atg	gac	gtc	tac	cag	145
Gly	Glu	Gln	Lys	Ala	His	Glu	Val	Val	Lys	Phe	Met	Asp	Val	Tyr	Gln	
			35				40						45			

cgc agc tat tgc cgt ccg att gag acc ctg gtg gac atc ttc cag gag 193
 Arg Ser Tyr Cys Arg Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
 50 55 60

tac ccc gat gag ata gag tat atc ttc aag ccg tcc tgt gtg ccc cta 241
 Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
 65 70 75

atg cgg tgt gcg ggc tgc tgc aat gat gaa gcc ctg gag tgc gtg ccc 289
 Met Arg Cys Ala Gly Cys Cys Asn Asp Glu Ala Leu Glu Cys Val Pro
 80 85 90 95

acg tcg gag agc aac gtc act atg cag atc atg cgg atc aaa cct cac 337
 Thr Ser Glu Ser Asn Val Thr Met Gln Ile Met Arg Ile Lys Pro His
 100 105 110

caa agc cag cac ata gga gag atg agc ttc ctg cag cat agc aga tgt 385
 Gln Ser Gln His Ile Gly Glu Met Ser Phe Leu Gln His Ser Arg Cys
 115 120 125

gaa tgc aga cca aag aaa gat aga aca aag cca gaa aat cac tgt gag 433
 Glu Cys Arg Pro Lys Lys Asp Arg Thr Lys Pro Glu Asn His Cys Glu
 130 135 140

cct tgt tca gag cgg aga aag cat ttg ttt gtc caa gat ccg cag acg 481
 Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr
 145 150 155

tgt aaa tgt tcc tgc aaa aac aca gac tcg cgt tgc aag gcg agg cag 529
 Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln
 160 165 170 175

ctt gag tta aac gaa cgt act tgc aga tgt gac aag cca agg cgg tga 577
 Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg *
 180 185 190

<210> 2
 <211> 190
 <212> PRT
 <213> rat

<400> 2
 Met Asn Phe Leu Leu Ser Trp Val His Trp Thr Leu Ala Leu Leu Leu
 1 5 10 15
 Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Thr Thr Glu Gly
 20 25 30
 Glu Gln Lys Ala His Glu Val Val Lys Phe Met Asp Val Tyr Gln Arg
 35 40 45
 Ser Tyr Cys Arg Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu Tyr
 50 55 60
 Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu Met
 65 70 75 80
 Arg Cys Ala Gly Cys Cys Asn Asp Glu Ala Leu Glu Cys Val Pro Thr
 85 90 95

Ser Glu Ser Asn Val Thr Met Gln Ile Met Arg Ile Lys Pro His Gln
 100 105 110
 Ser Gln His Ile Gly Glu Met Ser Phe Leu Gln His Ser Arg Cys Glu
 115 120 125
 Cys Arg Pro Lys Lys Asp Arg Thr Lys Pro Glu Asn His Cys Glu Pro
 130 135 140
 Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr Cys
 145 150 155 160
 Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln Leu
 165 170 175
 Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg
 180 185 190

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<211> 477

<212> DNA

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<222> (1)...(477)

<400> 3

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1 5 10 15	
ttg gct gtg cac tcc cag ggg gcc ctg tct gct ggg aac aac tca aca	96
Leu Ala Val His Ser Gln Gly Ala Leu Ser Ala Gly Asn Asn Ser Thr	
20 25 30	
gaa atg gaa gtg gtg cct ttc aat gaa gtg tgg ggc cgc agc tac tgc	144
Glu Met Glu Val Val Pro Phe Asn Glu Val Trp Gly Arg Ser Tyr Cys	
35 40 45	
cgg cca atg gag aag ctg gtg tac att gca gat gaa cac cct aat gaa	192
Arg Pro Met Glu Lys Leu Val Tyr Ile Ala Asp Glu His Pro Asn Glu	
50 55 60	
gtg tct cat ata ttc agt ccg tca tgt gtc ctt ctg agt cgc tgt agt	240
Val Ser His Ile Phe Ser Pro Ser Cys Val Leu Leu Ser Arg Cys Ser	
65 70 75 80	
ggc tgc tgt ggt gac gag ggt ctg cac tgt gtg gcg cta aag aca gcc	288
Gly Cys Cys Gly Asp Glu Gly Leu His Cys Val Ala Leu Lys Thr Ala	
85 90 95	
aac atc act atg cag atc tta aag att ccc ccc aat cgg gat cca cat	336
Asn Ile Thr Met Gln Ile Leu Lys Ile Pro Pro Asn Arg Asp Pro His	
100 105 110	
tcc tac gtg gag atg aca ttc tct cag gat gta ctc tgc gaa tgc agg	384
Ser Tyr Val Glu Met Thr Phe Ser Gln Asp Val Leu Cys Glu Cys Arg	
115 120 125	

cct att ctg gag acg aca aag gca gaa agg agg aaa acc aag ggg aag 432
 Pro Ile Leu Glu Thr Thr Lys Ala Glu Arg Arg Lys Thr Lys Gly Lys
 130 135 140

agg aag caa agc aaa acc cca cag act gag gaa ccc cac ctg tga 477
 Arg Lys Gln Ser Lys Thr Pro Gln Thr Glu Glu Pro His Leu *
 145 150 155

<210> 4
 <211> 158
 <212> PRT
 <213> rat

<400> 4
 Met Leu Ala Met Lys Leu Phe Thr Cys Phe Leu Gln Val Leu Ala Gly
 1 5 10 15
 Leu Ala Val His Ser Gln Gly Ala Leu Ser Ala Gly Asn Asn Ser Thr
 20 25 30
 Glu Met Glu Val Val Pro Phe Asn Glu Val Trp Gly Arg Ser Tyr Cys
 35 40 45
 Arg Pro Met Glu Lys Leu Val Tyr Ile Ala Asp Glu His Pro Asn Glu
 50 55 60
 Val Ser His Ile Phe Ser Pro Ser Cys Val Leu Leu Ser Arg Cys Ser
 65 70 75 80
 Gly Cys Cys Gly Asp Glu Gly Leu His Cys Val Ala Leu Lys Thr Ala
 85 90 95
 Asn Ile Thr Met Gln Ile Leu Lys Ile Pro Pro Asn Arg Asp Pro His
 100 105 110
 Ser Tyr Val Glu Met Thr Phe Ser Gln Asp Val Leu Cys Glu Cys Arg
 115 120 125
 Pro Ile Leu Glu Thr Thr Lys Ala Glu Arg Arg Lys Thr Lys Gly Lys
 130 135 140
 Arg Lys Gln Ser Lys Thr Pro Gln Thr Glu Glu Pro His Leu
 145 150 155

<210> 5
 <211> 417
 <212> DNA
 <213> rat

<220>
 <221> CDS
 <222> (1)...(417)

<400> 5
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 Met Leu Ala Met Lys Leu Phe Thr Cys Phe Leu Gln Val Leu Ala Gly
 1 5 10 15
 ttg gct gtg cac tcc cag ggg gcc ctg tct gct ggg aac aac tca aca 96
 Leu Ala Val His Ser Gln Gly Ala Leu Ser Ala Gly Asn Asn Ser Thr
 20 25 30

gaa atg gaa gtg gtg cct ttc aat gaa gtg tgg ggc cgc agc tac tgc 144
 Glu Met Glu Val Val Pro Phe Asn Glu Val Trp Gly Arg Ser Tyr Cys
 35 40 45

cgg cca atg gag aag ctg gtg tac att gca gat gaa cac cct aat gaa 192
 Arg Pro Met Glu Lys Leu Val Tyr Ile Ala Asp Glu His Pro Asn Glu
 50 55 60

gtg tct cat ata ttc agt ccg tca tgt gtc ctt ctg agt cgc tgt agt 240
 Val Ser His Ile Phe Ser Pro Ser Cys Val Leu Leu Ser Arg Cys Ser
 65 70 75 80

ggc tgc tgt ggt gac gag ggt ctg cac tgt gtg gcg cta aag aca gcc 288
 Gly Cys Cys Gly Asp Glu Gly Leu His Cys Val Ala Leu Lys Thr Ala
 85 90 95

aac atc act atg cag atc tta aag att ccc ccc aat cgg gat cca cat 336
 Asn Ile Thr Met Gln Ile Leu Lys Ile Pro Pro Asn Arg Asp Pro His
 100 105 110

tcc tac gtg gag atg aca ttc tct cag gat gta ctc tgc gaa tgc agg 384
 Ser Tyr Val Glu Met Thr Phe Ser Gln Asp Val Leu Cys Glu Cys Arg
 115 120 125

cct att ctg gag acg aca aag gca gaa agg taa 417
 Pro Ile Leu Glu Thr Thr Lys Ala Glu Arg *
 130 135

<210> 6

<211> 138

<212> PRT

<213> rat

<400> 6

Met Leu Ala Met Lys Leu Phe Thr Cys Phe Leu Gln Val Leu Ala Gly
 1 5 10 15
 Leu Ala Val His Ser Gln Gly Ala Leu Ser Ala Gly Asn Asn Ser Thr
 20 25 30
 Glu Met Glu Val Val Pro Phe Asn Glu Val Trp Gly Arg Ser Tyr Cys
 35 40 45
 Arg Pro Met Glu Lys Leu Val Tyr Ile Ala Asp Glu His Pro Asn Glu
 50 55 60
 Val Ser His Ile Phe Ser Pro Ser Cys Val Leu Leu Ser Arg Cys Ser
 65 70 75 80
 Gly Cys Cys Gly Asp Glu Gly Leu His Cys Val Ala Leu Lys Thr Ala
 85 90 95
 Asn Ile Thr Met Gln Ile Leu Lys Ile Pro Pro Asn Arg Asp Pro His
 100 105 110
 Ser Tyr Val Glu Met Thr Phe Ser Gln Asp Val Leu Cys Glu Cys Arg
 115 120 125
 Pro Ile Leu Glu Thr Thr Lys Ala Glu Arg
 130 135

<210> 7

<211> 14

<212> PRT

<213> rat

<400> 7

Ala Pro Thr Thr Glu Gly Glu Gln Lys Ala His Glu Val Val
1 5 10

<210> 8

<211> 19

<212> PRT

<213> rat

<220>

<221> MOD_RES

<222> (7)...(7)

<223> Xaa = Unknown

<400> 8

Ala Leu Ser Ala Gly Asn Xaa Ser Thr Glu Met Glu Val Val Pro Phe
1 5 10 15
Asn Glu Val

<210> 9

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<221> modified_base

<222> (0)...(0)

<223> n = t,c,g,a
y=t,c

<400> 9

tttgtcgact yatggaygtn tayca

25

<210> 10

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<221> modified_base

<222> (0)...(0)

<223> n = t,c,g,a
y = t,c
r = a,g

<400> 10

cagagaattc gtcgacartc ngtrtttyttr ca

32

<210> 11
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 11
gactcgagtc gacatcgatt tttttttttt ttttt 35

<210> 12
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 12
tttgtcgact cagagcggag aaagc 25

<210> 13
<211> 25
<212> DNA
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<220>
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<400> 13
tttgtcgacg aaaatcactg tgagc 25

<210> 14
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 14
gactcgagtc gacatcg 17

<210> 15
<211> 28
<212> DNA
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<220>
<223> oligonucleotide

<400> 15
tttgtcgaca acacaggacg gcttgaag 28

<210> 16
 <211> 28
 <212> DNA
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 <220>
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 <400> 16
 tttgtcgaca tactcctgga agatgtcc 28

 <210> 17
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 <220>
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 <400> 17
 cttcatcatt gcagcagc 18

 <210> 18
 <211> 26
 <212> DNA
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 <220>
 <223> oligonucleotide

 <400> 18
 tttgtcgaca accatgaact ttctgc 26

 <210> 19
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 <400> 19
 tttgtcgacg gtgagaggtc tagttc 26

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 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> oligonucleotide

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 aaaatcagtt cgaggaaagg gaaaggggtca aaaacgaaag cgcaagaaat cccggtttaa 60
 atcctggagc gt 72

<210> 21
 <211> 25
 <212> PRT
 <213> rat

<400> 21
 Lys Lys Ser Val Arg Gly Lys Gly Lys Gly Gln Lys Arg Lys Arg Lys
 1 5 10 15
 Lys Ser Arg Phe Lys Ser Trp Ser Val
 20 25

<210> 22
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide

<221> modified_base
 <222> (0)...(0)
 <223> n = t,c,g,a
 h = t,c,a
 y = t,c
 r = a,g

<400> 22
 tttgtcgaca tayathgcng aygarc 26

<210> 23
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide

<221> modified_base
 <222> (0)...(0)
 <223> n = t,c,g,a
 r = a,g

<400> 23
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<210> 24
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide

<400> 24

gactcgagtc gacatcgatt tttttttttt ttttt 35

<210> 25
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide

<400> 25
 tttgtcgaca caccctaagc aagtgctc 27

<210> 26
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide

<400> 26
 tttgtcgaca acagcgactc agaagg 26

<210> 27
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide

<400> 27
 tttgtcgaca ctgaatatat gagacac 27

<210> 28
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide

<221> modified_base
 <222> (0)...(0)
 <223> n = t,c,g,a

<400> 28
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<210> 29
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>

<223> oligonucleotide

<221> modified_base

<222> (0)...(0)

<223> n = t,c,g,a

<400> 29

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26